

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2005, 07:21:03 ; Search time 7823 Seconds
(without alignments)
10899.294 Million cell updates/sec

Title: US-10-787-267A-11

Perfect score: 1500

Sequence: 1 ctaaaaacaaggcacaataata.....ggccttctggctgggtattg 1500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_in:
3: gb_env:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pr:
9: gb_ro:
10: gb_sts:
11: gb_sy:
12: gb_un:
13: gb_vi:
14: gb_htg:
15: gb_pl:

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OM nucleic - nucleic search, using sw model

Run on: December 10, 2005, 21:20:20 ; Search time 968 Seconds
(without alignments)
10327.520 Million cell updates/sec

Title: US-10-787-267A-11

Perfect score: 1500

Sequence: 1 ctaaaaacaaggcacaataata.....ggccttctggctgggtattg 1500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:
14: geneseqn2005s:

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2005, 07:47:48 ; Search time 6467 Seconds
(without alignments)
10852.114 Million cell updates/sec

Title: US-10-787-267A-11
Perfect score: 1500
Sequence: 1 ctaaaaacaaggcacaataata.....ggccttctggctgggtattg 1500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_htc:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gss1:
10: gb_gss2:
11: gb_gss3:

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2005, 14:20:48 ; Search time 7821 Seconds
(without alignments)
10902.081 Million cell updates/sec

Title: US-10-787-267A-11

Perfect score: 1500

Sequence: 1 ctaaaaacaaggcacaataata.....ggccttctggctgggtattg 1500

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_in:*

3: gb_env:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pr:*

9: gb_ro:*

10: gb_sts:*

11: gb_sy:*

12: gb_un:*

13: gb_vi:*

14: gb_htg:*

15: gb_pl:*

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2005, 16:50:13 ; Search time 968 Seconds
(without alignments)
10327.520 Million cell updates/sec

Title: US-10-787-267A-11

Perfect score: 1500

Sequence: 1 ctaaaaacaaggcacaataata.....ggccttctggctgggtattg 1500

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_21:
1: geneseqn1980s:
2: geneseqn1990s:
3: geneseqn2000s:
4: geneseqn2001as:
5: geneseqn2001bs:
6: geneseqn2002as:
7: geneseqn2002bs:
8: geneseqn2003as:
9: geneseqn2003bs:
10: geneseqn2003cs:
11: geneseqn2003ds:
12: geneseqn2004as:
13: geneseqn2004bs:
14: geneseqn2005s:

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2005, 16:50:49 ; Search time 6467 Seconds
(without alignments)
10852.114 Million cell updates/sec

Title: US-10-787-267A-11
Perfect score: 1500
Sequence: 1 ctaaaaacaaggcacaataata.....ggccttctggctgggtattg 1500

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_htc:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gss1:
10: gb_gss2:
11: gb_gss3:

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OM protein - protein search, using sw model

Run on: December 7, 2005, 10:21:57 ; Search time 187 Seconds

(without alignments)
1031.483 Million cell updates/sec

Title: US-10-787-267A-12
Perfect score: 2254
Sequence: 1 MNITSNSTTKDIPRQRWLRI.....AKCDAGAAPVKTINPHKRTA 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:
9: geneseqp2005s:

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OM protein - protein search, using sw model

Run on: December 7, 2005, 10:23:28 ; Search time 39 Seconds
(without alignments)
1083.055 Million cell updates/sec

Title: US-10-787-267A-12
Perfect score: 2254
Sequence: 1 MNITSNSTTKDIPRQRWLRI.....AKCDAGAAPVKTINPHKRTA 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 7, 2005, 10:22:48 ; Search time 228 Seconds
(without alignments)
1358.451 Million cell updates/sec

Title: US-10-787-267A-12

Perfect score: 2254

Sequence: 1 MNITSNSTTKDIPRQRWLRI.....AKCDAGAAPVKTINPHKRTA 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*